

0590  
1205

#2

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/884,566

DATE: 11/27/2001

TIME: 19:21:21

Input Set : N:\Cr3\RULE60\09884566.raw

Output Set: N:\CRF3\11272001\I884566.raw

SEQUENCE LISTING

ENTERED

1 (1) GENERAL INFORMATION:  
2 (i) APPLICANT: Keegan, Kathleen S.  
3 (ii) TITLE OF INVENTION: Novel CREBa Isoform  
4 (iii) NUMBER OF SEQUENCES: 10  
5 (iv) CORRESPONDENCE ADDRESS:  
6 (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
7 (B) STREET: 233 South Wacker Drvie, 6300 Sears Tower  
8 (C) CITY: Chicago  
9 (D) STATE: Illinois  
10 (E) COUNTRY: USA  
11 (F) ZIP: 60606  
12 (v) COMPUTER READABLE FORM:  
13 (A) MEDIUM TYPE: Floppy disk  
14 (B) COMPUTER: IBM PC compatible  
15 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
16 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
17 (vi) CURRENT APPLICATION DATA:  
C--> 18 (A) APPLICATION NUMBER: US/09/884,566  
C--> 19 (B) FILING DATE: 19-Jun-2001  
20 (vii) PRIOR APPLICATION DATA:  
21 (A) APPLICATION NUMBER: US/09/407,715  
22 (B) FILING DATE: 28-Sep-1999  
23 (A) APPLICATION NUMBER: US/09/005,970  
24 (B) FILING DATE: 12-JAN-1998  
25 (A) APPLICATION NUMBER: US/08/721,684  
26 (B) FILING DATE: 27-SEP-1996  
27 (viii) ATTORNEY/AGENT INFORMATION:  
28 (A) NAME: Williams Jr., Joseph A.  
29 (B) REGISTRATION NUMBER: 38,659  
30 (C) REFERENCE/DOCKET NUMBER: 27866/33487  
31 (ix) TELECOMMUNICATION INFORMATION:  
32 (A) TELEPHONE: 312-474-6300  
33 (B) TELEFAX: 312-474-0448  
34 (2) INFORMATION FOR SEQ ID NO: 1:  
35 (i) SEQUENCE CHARACTERISTICS:  
36 (A) LENGTH: 3190 base pairs  
37 (B) TYPE: nucleic acid  
38 (C) STRANDEDNESS: single  
39 (D) TOPOLOGY: linear  
40 (ii) MOLECULE TYPE: cDNA  
41 (ix) FEATURE:  
42 (A) NAME/KEY: CDS  
43 (B) LOCATION: 304..1866  
44 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
45 GGCACGAGGG ACTTTCTTGG GATGAGCGCT GCCTTTTTTGG CTTCTTTTGG GATGCACAGC 60  
46 CCGATTAAAC CCCTGCACCT TCCGCCCGAT CCCAGCAGGC TTGTCCTCCC CGGGGAGTCA 120

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47	CAGATTTC	CGG	AGGACAAGGG	TCGCGTAGCC	TTCGGCAGGG	CTCTCCCGAG	TTCCTGCTCC	180									
48	AGTGCATAAG	TTCCACGCGC	GCACACGCCA	AGTACACGGG	GAGAAGCGTC	TCACCGGCC	240										
49	GCGGCGGCTC	TGCGCGGTCC	CCTCCTGCCT	CAGCATCCTC	GGGCCTGCGC	GGCGCCCACC	300										
50	GCC	ATG	GAG	GTG	CTG	GAG	AGC	GGG	GAG	CAG	AGC	GTC	CTG	CAG	TGG	GAC	348
51	Met	Glu	Val	Leu	Glu	Ser	Gly	Glu	Gln	Ser	Val	Leu	Gln	Trp	Asp		
52	1				5					10					15		
53	CGC	AAG	CTG	AGC	GAG	CTG	TCA	GAG	CCC	GGA	GAG	ACT	GAG	GCC	CTC	ATG	396
54	Arg	Lys	Leu	Ser	Glu	Leu	Ser	Glu	Pro	Gly	Glu	Thr	Glu	Ala	Leu	Met	
55				20					25					30			
56	TAC	CAC	ACG	CAC	TTC	TCG	GAG	CTC	CTA	GAC	GAG	TTT	TCC	CAG	AAC	GTC	444
57	Tyr	His	Thr	His	Phe	Ser	Glu	Leu	Leu	Asp	Glu	Phe	Ser	Gln	Asn	Val	
58				35				40					45				
59	CTG	GGT	CAG	CTC	CTG	AGT	GAC	CCT	TTC	CTC	TCA	GAG	AAG	AGC	GAG	TCA	492
60	Leu	Gly	Gln	Leu	Leu	Ser	Asp	Pro	Phe	Leu	Ser	Glu	Lys	Ser	Glu	Ser	
61		50				55					60						
62	ATG	GAG	GTG	GAG	CCA	TCT	CCA	ACA	TCA	CCA	GCG	CCT	CTC	ATC	CAG	GCT	540
63	Met	Glu	Val	Glu	Pro	Ser	Pro	Thr	Ser	Pro	Ala	Pro	Leu	Ile	Gln	Ala	
64		65				70					75						
65	GAA	CAC	AGC	TAC	TCT	CTG	AGC	GAG	GAG	CCC	CGG	ACT	CAG	TCA	CCA	TTT	588
66	Glu	His	Ser	Tyr	Ser	Leu	Ser	Glu	Glu	Pro	Arg	Thr	Gln	Ser	Pro	Phe	
67		80				85				90				95			
68	ACC	CAT	GCG	GCT	ACC	AGC	GAC	AGC	TTC	AAT	GAC	GAG	GAG	GTG	GAG	AGT	636
69	Thr	His	Ala	Ala	Thr	Ser	Asp	Ser	Phe	Asn	Asp	Glu	Glu	Val	Glu	Ser	
70				100					105					110			
71	GAA	AAA	TGG	TAC	CTG	TCT	ACA	GAG	TTT	CCT	TCA	GCT	ACC	ATC	AAG	AAA	684
72	Glu	Lys	Trp	Tyr	Leu	Ser	Thr	Glu	Phe	Pro	Ser	Ala	Thr	Ile	Lys	Lys	
73				115					120					125			
74	GAG	CCA	ATC	ACA	GAG	GAG	CAG	CCC	CCG	GGA	CTT	GTC	CCT	TCT	GTC	ACT	732
75	Glu	Pro	Ile	Thr	Glu	Glu	Gln	Pro	Pro	Gly	Leu	Val	Pro	Ser	Val	Thr	
76				130				135					140				
77	CTG	ACC	ATC	ACA	GCC	ATT	TCC	ACT	CCT	TTT	GAA	AAA	GAA	GAG	TCC	CCT	780
78	Leu	Thr	Ile	Thr	Ala	Ile	Ser	Thr	Pro	Phe	Glu	Lys	Glu	Glu	Ser	Pro	
79		145				150					155						
80	CTG	GAT	ATG	AAT	GCT	GGG	GGG	GAC	TCC	TCA	TGC	CAG	ACG	CTT	ATT	CCT	828
81	Leu	Asp	Met	Asn	Ala	Gly	Gly	Asp	Ser	Ser	Cys	Gln	Thr	Leu	Ile	Pro	
82		160				165					170				175		
83	AAG	ATT	AAG	CTG	GAG	CCC	CAC	GAA	GTG	GAT	CAG	TTC	TTA	AAC	TTC	TCC	876
84	Lys	Ile	Lys	Leu	Glu	Pro	His	Glu	Val	Asp	Gln	Phe	Leu	Asn	Phe	Ser	
85				180					185					190			
86	CCG	AAA	GAA	GCC	TCC	GTG	GAT	CAA	CTG	CAC	TTA	CCA	CCA	ACA	CCA	CCC	924
87	Pro	Lys	Glu	Ala	Ser	Val	Asp	Gln	Leu	His	Leu	Pro	Pro	Thr	Pro	Pro	
88				195				200					205				
89	AGT	AGT	CAC	AGC	AGT	GAC	TCT	GAG	GGC	AGC	TTG	AGC	CCC	AAC	CCA	CGC	972
90	Ser	Ser	His	Ser	Ser	Asp	Ser	Glu	Gly	Ser	Leu	Ser	Pro	Asn	Pro	Arg	
91				210				215					220				
92	CTG	CAT	CCC	TTC	AGC	CTG	TCT	CAG	GCC	CAC	AGC	CCT	GTC	AGA	GCC	ATG	1020
93	Leu	His	Pro	Phe	Ser	Leu	Ser	Gln	Ala	His	Ser	Pro	Val	Arg	Ala	Met	
94				225				230					235				
95	CCC	CGG	GGC	CCC	TCT	GCC	TTG	TCC	ACA	TCT	CCT	CTC	CTC	ACA	GCT	CCA	1068

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96	Pro Arg Gly Pro Ser Ala Leu Ser Thr Ser Pro Leu Leu Thr Ala Pro	
97	240 245 250 255	
98	CAT AAG CTG CAG GGA TCG GGC CCC CTG GTC CTG ACA GAA GAG GAG AAG	1116
99	His Lys Leu Gln Gly Ser Gly Pro Leu Val Leu Thr Glu Glu Glu Lys	
100	260 265 270	
101	AGG ACC CTG GTT GCC GAG GGC TAT CCC ATT CCC ACC AAG CTG CCT CTG	1164
102	Arg Thr Leu Val Ala Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu	
103	275 280 285	
104	ACA AAA TCT GAG GAG AAG GCC CTG AAG AAA ATC CGG AGA AAG ATC AAG	1212
105	Thr Lys Ser Glu Glu Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys	
106	290 295 300	
107	AAT AAG ATT TCT GCC CAA GAA AGC AGG AGA AAG AAG AAA GAA TAC ATG	1260
108	Asn Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys Lys Glu Tyr Met	
109	305 310 315	
110	GAC AGC CTG GAG AAA AAA GTG GAG TCT TGT TCA ACT GAG AAC TTG GAG	1308
111	Asp Ser Leu Glu Lys Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu	
112	320 325 330 335	
113	CTT CGG AAG AAG GTG GAG GTG CTG GAG AAC ACC AAT AGG ACT CTC CTT	1356
114	Leu Arg Lys Lys Val Glu Val Leu Glu Asn Thr Asn Arg Thr Leu Leu	
115	340 345 350	
116	CAG CAA CTT CAG AAG CTT CAG ACT TTG GTG ATG GGG AAG GTC TCT CGA	1404
117	Gln Gln Leu Gln Lys Leu Gln Thr Leu Val Met Gly Lys Val Ser Arg	
118	355 360 365	
119	ACC TGC AAG TTA GCT GGC ACA CAG ACT GGC ACC TGC CTC ATG GTC GTT	1452
120	Thr Cys Lys Leu Ala Gly Thr Gln Thr Gly Thr Cys Leu Met Val Val	
121	370 375 380	
122	GTG CTT TGC TTT GCT GTT GCA TTT GGA AGC TTC TTT CAA GGC TAT GGG	1500
123	Val Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly	
124	385 390 395	
125	CCT TAT CCT TCT GCC ACC AAG ATG GCT CTG CCC AGC CAG CAT CCT CTG	1548
126	Pro Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu	
127	400 405 410 415	
128	TCA GAG CCA TAC ACA GCC TCC GTG GTG AGA TCC AGG AAC CTG CTA ATC	1596
129	Ser Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile	
130	420 425 430	
131	TAT GAG GAA CAC GCT CCC CTG GAA GAG TCG AGC CCA GCC TCA ACC	1644
132	Tyr Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr	
133	435 440 445	
134	GGG GAG CTG GGG GGC TGG GAC AGA GGC TCC TCT CTG CTC AGG GCA TCG	1692
135	Gly Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser	
136	450 455 460	
137	TCG GGG CTT GAG GCC CTG CCA GAG GTG GAT CTT CCC CAT TTC CTT ATC	1740
138	Ser Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile	
139	465 470 475	
140	TCC AAT GAG ACG AGC TTG GAG AAG TCA GTA CTG TTG GAG CTT CAG CAG	1788
141	Ser Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln	
142	480 485 490 495	
143	CAC CTG GTC AGC AGC AAA CTG GAA GGG AAC GAA ACA CTC AAG GTT GTA	1836
144	His Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val	

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145		500		505		510	
146	GAG CTG GAG AGG AGA GTG AAC GCC ACC TTC TGAGGAGAGC TCCACCCTCC						1886
147	Glu Leu Glu Arg Arg Val Asn Ala Thr Phe						
148		515		520			
149	TCTTCTCCTA ACTCCATCTG ATCGTCCTTT CAGTTTCCCC TTCACCACTG GATCTCGAGG						1946
150	AGGAGATGGC TAGTGTTACG GCTCGAGACA GGAGGCCAGC CCAGGGGGTT CTGCTTATGT						2006
151	GTCCCCGTGG CTCTCCACAA AAGGGAGCTA GCACCTCTCC ATCCCTTTCT CTTACTGCCA						2066
152	TTGGAAATTA TTTTAGGGCT GAGATAGGGG TGGAACGAGC AGGCTTGTTT CCACCAATAG						2126
153	TGCCAAGAAG AACTGCCTG ATTCTTCCCC GGGAGGAGTG ACTCCTCTGA AGAAGACATG						2186
154	ACTCATGTTT AGTTGAGACC CCAGACTCTA GCCACACACA TGCCACAGAC ATGCCAGGGA						2246
155	GTGGCAAAGC ACTGACTCCT GAGCTCCCTT CCTCACTAGG ACTCCAGTGT GACCCTGCAC						2306
156	TGAGAGGACC AAAGCGTCAT TGCAGTCTTC TCTCCACCCT GTACCCCGGA GTCCTGATTG						2366
157	GATGTCTGCA GAGGCAGATG GGGCTCCAC CATATTTTCA GGCCGCAAGT GCAATTCCTG						2426
158	AAGGCATCAG GCTCTTCTCT CCCAGGCTCT CCTGCCACT GTGTTGTTTG TAGGACACCC						2486
159	CCACACCCAC TCATACACAG CCTGCATCTC CACAGGACAA TAGCTCTGTC TCCCTGGCCT						2546
160	CCCCTCCCCA TTTGTAAATA GTATTTATTA GCTTGCTCAA GCTCCCAGCT GGCCATAGTG						2606
161	AAAAGATTTT CCCTTTCAAC CAGCAAAGTC TTCTGTTGGC CTTTGAACA GGAGAGTCCC						2666
162	CGGAATCTAG GACCCTAGTC TTTGTACTTG ATGCCTTGTT TCCCCCTTT TCTTCTTTAA						2726
163	AATTGGGGAC CTATAACATC ATCGCTGTTG CGGAATCCAC TTAGGCATGT GTCCCCTGAT						2786
164	GGATGAATAC ATGGGAATGG TGGATACTGT CTTCTGACTC AGGCTCTAGG CTCCATGGCT						2846
165	TCCTCTCTCT GGTCTGCCA CACAGAAGGA AAGCCCTGTC CAGGATAATG AGCGTTGCTG						2906
166	ACACCCTTGC TAGCTTGTC TGCCTACCTG CTTACCCAC TCCCTCACCT TCCTCCTTCC						2966
167	CTTCTGCCCT CCATCCACCT GCCTTAACTA ATTGGGGCTG GAGTTGGTCA TTTTTGTAC						3026
168	ACCCACAGTG GTACCTTTTA CAGTCAGGTT TGGATACTTT GCAGCTCATC CAAAGAGACA						3086
169	TAATAAACC CTAAACTCTT TTTTGTGTTG TGTTGTTGTT GTTTTTTTTT TTTATGATTA						3146
170	AAAAGTAAAA ATTGTAGTTT AAAAAAAAAA AAAAAAACT CGAG						3190
172	(2) INFORMATION FOR SEQ ID NO: 2:						
173	(i) SEQUENCE CHARACTERISTICS:						
174	(A) LENGTH: 521 amino acids						
175	(B) TYPE: amino acid						
176	(D) TOPOLOGY: linear						
177	(ii) MOLECULE TYPE: protein						
178	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:						
179	Met Glu Val Leu Glu Ser Gly Glu Gln Ser Val Leu Gln Trp Asp Arg						
180	1 5 10 15						
181	Lys Leu Ser Glu Leu Ser Glu Pro Gly Glu Thr Glu Ala Leu Met Tyr						
182	20 25 30						
183	His Thr His Phe Ser Glu Leu Leu Asp Glu Phe Ser Gln Asn Val Leu						
184	35 40 45						
185	Gly Gln Leu Leu Ser Asp Pro Phe Leu Ser Glu Lys Ser Glu Ser Met						
186	50 55 60						
187	Glu Val Glu Pro Ser Pro Thr Ser Pro Ala Pro Leu Ile Gln Ala Glu						
188	65 70 75 80						
189	His Ser Tyr Ser Leu Ser Glu Glu Pro Arg Thr Gln Ser Pro Phe Thr						
190	85 90 95						
191	His Ala Ala Thr Ser Asp Ser Phe Asn Asp Glu Glu Val Glu Ser Glu						
192	100 105 110						
193	Lys Trp Tyr Leu Ser Thr Glu Phe Pro Ser Ala Thr Ile Lys Lys Glu						
194	115 120 125						

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195   Pro Ile Thr Glu Glu Gln Pro Pro Gly Leu Val Pro Ser Val Thr Leu
196       130                      135                      140
197   Thr Ile Thr Ala Ile Ser Thr Pro Phe Glu Lys Glu Glu Ser Pro Leu
198   145                      150                      155                      160
199   Asp Met Asn Ala Gly Gly Asp Ser Ser Cys Gln Thr Leu Ile Pro Lys
200       165                      170                      175
201   Ile Lys Leu Glu Pro His Glu Val Asp Gln Phe Leu Asn Phe Ser Pro
202       180                      185                      190
203   Lys Glu Ala Ser Val Asp Gln Leu His Leu Pro Pro Thr Pro Pro Ser
204       195                      200                      205
205   Ser His Ser Ser Asp Ser Glu Gly Ser Leu Ser Pro Asn Pro Arg Leu
206       210                      215                      220
207   His Pro Phe Ser Leu Ser Gln Ala His Ser Pro Val Arg Ala Met Pro
208   225                      230                      235                      240
209   Arg Gly Pro Ser Ala Leu Ser Thr Ser Pro Leu Leu Thr Ala Pro His
210       245                      250                      255
211   Lys Leu Gln Gly Ser Gly Pro Leu Val Leu Thr Glu Glu Glu Lys Arg
212       260                      265                      270
213   Thr Leu Val Ala Glu Gly Tyr Pro Ile Pro Thr Lys Leu Pro Leu Thr
214       275                      280                      285
215   Lys Ser Glu Glu Lys Ala Leu Lys Lys Ile Arg Arg Lys Ile Lys Asn
216       290                      295                      300
217   Lys Ile Ser Ala Gln Glu Ser Arg Arg Lys Lys Lys Glu Tyr Met Asp
218   305                      310                      315                      320
219   Ser Leu Glu Lys Lys Val Glu Ser Cys Ser Thr Glu Asn Leu Glu Leu
220       325                      330                      335
221   Arg Lys Lys Val Glu Val Leu Glu Asn Thr Asn Arg Thr Leu Leu Gln
222       340                      345                      350
223   Gln Leu Gln Lys Leu Gln Thr Leu Val Met Gly Lys Val Ser Arg Thr
224       355                      360                      365
225   Cys Lys Leu Ala Gly Thr Gln Thr Gly Thr Cys Leu Met Val Val Val
226       370                      375                      380
227   Leu Cys Phe Ala Val Ala Phe Gly Ser Phe Phe Gln Gly Tyr Gly Pro
228   385                      390                      395                      400
229   Tyr Pro Ser Ala Thr Lys Met Ala Leu Pro Ser Gln His Pro Leu Ser
230       405                      410                      415
231   Glu Pro Tyr Thr Ala Ser Val Val Arg Ser Arg Asn Leu Leu Ile Tyr
232       420                      425                      430
233   Glu Glu His Ala Pro Leu Glu Glu Ser Ser Ser Pro Ala Ser Thr Gly
234       435                      440                      445
235   Glu Leu Gly Gly Trp Asp Arg Gly Ser Ser Leu Leu Arg Ala Ser Ser
236       450                      455                      460
237   Gly Leu Glu Ala Leu Pro Glu Val Asp Leu Pro His Phe Leu Ile Ser
238   465                      470                      475                      480
239   Asn Glu Thr Ser Leu Glu Lys Ser Val Leu Leu Glu Leu Gln Gln His
240       485                      490                      495
241   Leu Val Ser Ser Lys Leu Glu Gly Asn Glu Thr Leu Lys Val Val Glu
242       500                      505                      510
243   Leu Glu Arg Arg Val Asn Ala Thr Phe

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## VERIFICATION SUMMARY

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Input Set : N:\CrF3\RULE60\09884566.raw

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L:18 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:19 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:252 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3  
L:262 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4  
L:272 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5  
L:282 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6  
L:292 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7  
L:304 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8  
L:314 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9  
L:324 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10